

Serial Number: 09/720,096

☐ Changed a file from non-ASCII to ASCII

ENTERED

(PCT 09)

☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.☐ Edited a format error in the Current Application Data section, specifically:

Paper No. 10

DS 3/19/02

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____☐ Added the mandatory heading and subheadings for "Current Application Data".☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.☐ Inserted colons after headings/subheadings. Headings edited included: _____☐ Deleted extra, invalid, headings used by an applicant, specifically: _____☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____☐ Inserted mandatory headings, specifically: _____☐ Corrected an obvious error in the response, specifically: _____☐ Edited identifiers where upper case is used but lower case is required, or vice versa.☐ Corrected an error in the Number of Sequences field, specifically: _____☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

PCT09

RAW SEQUENCE LISTING DATE: 03/06/2001
 PATENT APPLICATION: US/09/720,096 TIME: 13:30:07

Input Set : A:\Cpg.pto
 Output Set: N:\CRF3\03062001\I720096.raw

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5 <110> APPLICANT: Dan Nilsson
6   Thomas Janzen
8 <120> TITLE OF INVENTION: Method of preventing bacteriophage
9   infection of bacterial cultures
12 <130> FILE REFERENCE: 21134 PC 1
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/720,096
C--> 14 <141> CURRENT FILING DATE: 2000-12-21
14 <150> PRIOR APPLICATION NUMBER: PA 1998 00878
15 <151> PRIOR FILING DATE: 1998-07-03
17 <150> PRIOR APPLICATION NUMBER: US 60/091,735
18 <151> PRIOR FILING DATE: 1998-07-06
20 <160> NUMBER OF SEQ ID NOS: 6
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 32
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with
31   deletion in thyA from strain CHCC373
33 <400> SEQUENCE: 1
34   tataatctgc agggtcacac tatcagtaat tg 32
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 33
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with
43   deletion in thyA from strain CHCC373
45 <400> SEQUENCE: 2
46   tattttaagc ttcacagtct gctattttga ttc 33
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 32
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with
55   deletion in thyA from strain CHCC373
57 <400> SEQUENCE: 3
58   taaattaagc ttcgcagaca agatttttaa ac 32
61 <210> SEQ ID NO: 4
62 <211> LENGTH: 32
63 <212> TYPE: DNA
64 <213> ORGANISM: Artificial Sequence
66 <220> FEATURE:
67 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with
68   deletion in thyA from strain CHCC373

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/720,096

DATE: 03/06/2001
TIME: 13:30:07

Input Set : A:\Cpg.pto
Output Set: N:\CRF3\03062001\I720096.raw

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70 <400> SEQUENCE: 4
71      atttaagtcg acgggtcata gtccacaagt tc 32
73 <210> SEQ ID NO: 5
74 <211> LENGTH: 18
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: Sequencing primer used for the verification of the
80      construction of plasmid with deletion in thyA from
81      strain CHCC373.
83 <400> SEQUENCE: 5
84      gactgttgcc ccatagcg 18
86 <210> SEQ ID NO: 6
87 <211> LENGTH: 20
88 <212> TYPE: DNA
89 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Sequencing primer used for the verification of the
93      construction of plasmid with deletion in thyA from
94      strain CHCC373.
96 <400> SEQUENCE: 6
97      gcttcgattt tagtatatgg 20
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/720,096

DATE: 03/06/2001

TIME: 13:30:08

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\03062001\I720096.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

PCT 09

RAW SEQUENCE LISTING DATE: 02/22/2001
 PATENT APPLICATION: US/09/720,096 TIME: 09:42:35

Input Set : A:\Sequence List.asc
 Output Set: N:\CRF3\02222001\I720096.raw

6 <110> APPLICANT: Dan Nilsson
 7 Thomas Janzen
 9 <120> TITLE OF INVENTION: Method of preventing bacteriophage
 10 infection of bacterial cultures
 13 <130> FILE REFERENCE: 21134 PC 1
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/720,096
 C--> 15 <141> CURRENT FILING DATE: 2000-12-21
 15 <150> PRIOR APPLICATION NUMBER: PA 1998 00878
 16 <151> PRIOR FILING DATE: 1998-07-03
 18 <150> PRIOR APPLICATION NUMBER: US 60/091,735
 19 <151> PRIOR FILING DATE: 1998-07-06
 21 <160> NUMBER OF SEQ ID NOS: 6
 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 32
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with
 32 deletion in thyA from strain CHCC373
 34 <400> SEQUENCE: 1
 W--> 35 tataatctgc agggtcacac tatcagtaat tg
 E--> 36 32
 38 <210> SEQ ID NO: 2
 39 <211> LENGTH: 33
 40 <212> TYPE: DNA
 41 <213> ORGANISM: Artificial Sequence
 43 <220> FEATURE:
 44 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with
 45 deletion in thyA from strain CHCC373
 47 <400> SEQUENCE: 2
 W--> 48 tattttaagc ttcacagtct gctattttga ttc
 E--> 49 33
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 32
 53 <212> TYPE: DNA
 54 <213> ORGANISM: Artificial Sequence
 56 <220> FEATURE:
 57 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with
 58 deletion in thyA from strain CHCC373
 60 <400> SEQUENCE: 3
 W--> 61 taaattaagc ttgcagaca agatttttaa ac
 E--> 62 32

Does Not Comply
 Corrected Diskette Needed

"Wrapped" Nucleics
 End of line nucleic
 numbers "wrapped"
 down to next line.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/720,096

DATE: 02/22/2001
TIME: 09:42:35

Input Set : A:\Sequence List.asc
Output Set: N:\CRF3\02222001\I720096.raw

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65 <210> SEQ ID NO: 4
66 <211> LENGTH: 32
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with
72 deletion in thyA from strain CHCC373
74 <400> SEQUENCE: 4
W--> 75 atttaagtgc acggtccata gtccacaagt tc
E--> 76 32
87 <210> SEQ ID NO: 5
88 <211> LENGTH: 18
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Sequencing primer used for the verification of
93 the
94 construction of plasmid with deletion in thyA
95 from
96 strain CHCC373.
97 <400> SEQUENCE: 5
W--> 98 gactgttgcc ccatagcg
E--> 99 18
100 <210> SEQ ID NO: 6
101 <211> LENGTH: 20
102 <212> TYPE: DNA
103 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Sequencing primer used for the verification of
106 the
107 construction of plasmid with deletion in thyA
108 from
109 strain CHCC373.
110 <400> SEQUENCE: 6
W--> 111 gcttcgattt tagtatatgg
E--> 112 20
113 Path: DOCSOPEN\WASHINGT\08360\54337\000009\42Y001!.DOC
114 doc #: 190440; v. 1
115 doc name: sequence List (54337.9)

```

wrapped nucleic number refer to p1

Text is "wrapped" down, over the limit of 4 lines for <223>

wrapped nucleic number

Text is "wrapped" down, over limit of 4 lines. for <223>

wrapped nucleic number

↘ Delete extraneous material from the end of the file.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/720,096

DATE: 02/22/2001

TIME: 09:42:36

Input Set : A:\Sequence List.asc

Output Set: N:\CRF3\02222001\I720096.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
 L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:35 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:36 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:36 M:252 E: No. of Seq. differs, <211>LENGTH:Input:32 Found:0 SEQ:1
 L:48 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:49 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:49 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:0 SEQ:2
 L:61 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:62 M:252 E: No. of Seq. differs, <211>LENGTH:Input:32 Found:0 SEQ:3
 L:75 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:76 M:252 E: No. of Seq. differs, <211>LENGTH:Input:32 Found:0 SEQ:4
 L:88 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
 L:91 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:92 M:252 E: No. of Seq. differs, <211>LENGTH:Input:18 Found:0 SEQ:5
 L:104 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
 L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
 L:110 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
 L:111 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:8 SEQ:6
 L:111 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
 L:111 M:112 C: (48) String data converted to lower case,
 L:112 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
 L:112 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
 L:112 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
 M:254 Repeated in SeqNo=6
 L:112 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:18
 M:112 Repeated in SeqNo=6
 L:112 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:31 SEQ:6